O PAGE: 1

46

RAW SEQUENCE LISTING PATENT APPLICATION US/09/265,606

DATE: 01/14/2000 TIME: 17:23:58

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This Raw Listing contains the General Information Section and up to the first 5 pages.

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SEQUENCE LISTING 1 2 3 (1) General Information: 4 5 (i) APPLICANT: Zimmermann, Rainer; Park, John E.; Rettig, Wolfgang; Old, Lloyd J. 6 7 (ii) TITLE OF INVENTION: ISOLATED DIMERIC FIBROBLAST ACTIVATION PROTEIN 8 ALPHA, AND USES THEREOF 9 10 11 (iii) NUMBER OF SEQUENCES: 10 12 (iv) CORRESPONDENCE ADDRESS: 13 (A) ADDRESSEE: Felfe & Lynch 14 (B) STREET: 805 Third Avenue 15 (C) CITY: New York City 16 17 (D) STATE: New York 18 (E) COUNTRY: USA (F) ZIP: 10022 19 20 (v) COMPUTER READABLE FORM: 21 (A) MEDIUM TYPE: Diskette, 3.5 inch, 2.0 MB storage 22 (B) COMPUTER: IBM PS/2 23 (C) OPERATING SYSTEM: PC-DOS 24 (D) SOFTWARE: Wordperfect 25 26 (vi) CURRENT APPLICATION DATA: 27 (A) APPLICATION NUMBER: 09/265,606 28 (B) FILING DATE: 29 (C) CLASSIFICATION: 30 31 (vii) PRIOR APPLICATION DATA: 32 (A) APPLICATION NUMBER: US/08/619, 280 33 34 (B) FILING DATE: 18-MARCH-1996 35 36 (A) APPLICATION NUMBER: 08/230,491 37 (B) FILING DATE: 20-APRIL-1994 38 (viii) ATTORNEY/AGENT INFORMATION: 39 (A) NAME: Hanson, Norman D. 40 (B) REGISTRATION NUMBER: 30,946 41 42 (C) REFERENCE/DOCKET NUMBER: LUD 5330.1 43 44 (ix) TELECOMMUNICATION INFORMATION: (A) TELEPHONE: (212) 688-9200 45

(B) TELEFAX: (212) 838-3884

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(2) INFORMATION FOR SEQ ID NO: 1:
      (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 2815 Base pairs (B) TYPE: nucleic acid
49
50
               (C) STRANDEDNESS: double
51
               (D) TOPOLOGY: linear
52
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
53
54
55
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56
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57
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58
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    TGCAGATAAC AATATAGTAC TTTATAATAT TGAAACAGGA CAATCATATA CCATTTTGAG 480
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    TGTATATCTA GAAAGTGATT ATTCAAAGCT TTGGAGATAC TCTTACACAG CAACATATTA 600
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67
720
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TCTCTGGTGG TCTCCTAATG GAAAATTTTT GGCATATGCG GAATTTAATG ATAAGGATAT 900
ACCAGTTATT GCCTATTCCT ATTATGGCGA TGAACAATAT CCTAGAACAA TAAATATTCC 960
72 ATACCCAAAG GCTGGAGCTA AGAATCCCGT TGTTCGGATA TTTATTATCG ATACCACTTA 1020
73 CCCTGCGTAT GTAGGTCCCC AGGAAGTGCC TGTTCCAGCA ATGATAGCCT CAAGTGATTA 1080
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81 CTATCCTCCA AGCAAGAAGT GTGTTACTTG CCATCTAAGG AAAGAAAGGT GCCAATATTA 1560
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85 TGAAGTAGAT GAAATTACTT TATGGTACAA GATGATTCTT CCTCCTCAAT TTGACAGATC 1800
   AAAGAAGTAT CCCTTGCTAA TTCAAGTGTA TGGTGGTCCC TGCAGTCAGA GTGTAAGGTC 1860
    TGTATTTGCT GTTAATTGGA TATCTTATCT TGCAAGTAAG GAAGGGATGG TCATTGCCTT 1920
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    GCTGGGTGTT TATGAAGTTG AAGACCAGAT TACAGCTGTC AGAAAATTCA TAGAAATGGG 2040
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98 ATCTGAAAAC CTTATATAAA CCCCTCAGAC AGTTTGCTTA TTTTATTTTT TATGTTGTAA 2580
99
    AATGCTAGTA TAAACAAACA AATTAATGTT GTTCTAAAGG CTGTTAAAAA AAAGATGAGG 2640
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100 101 102 103 104 105	ACTCAGAAGT TCAAGCTAAA TATTGTTTAC ATTTTCTGGT ACTCTGTGAA AGAAGAGAAA 2700 AGGGAGTCAT GCATTTTGCT TTGGACACAG TGTTTTATCA CCTGTTCATT TGAAGAAAAA 2760 TAATAAAGTC AGAAGTTCAA AAAAAAAAAA AAAAAAAAAA																
106 107 108	(2)) SE	QUEN		SEQ HARA	CTER	ISTI		aide							
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111		(xi	•			ESCR:			S	EQ I	D NO	: 2:					
112																	
113																	
114	Met	Lys	Thr	Trp	Val	Lys	Ile	Val	Phe	Gly	Val	Ala	Thr	Ser	Ala	Val	
115					5					10					15		
116			_		-		_			_	_	_	_	_			
117	Leu	Ala	Leu		Val	Met	Cys	Ile		Leu	Arg	Pro	Ser		Val	His	
118				20					25					30			
119	7.00	Cor	C1.,	C1,,	7 cn	Thr	Mot	7 ~~	ת 1 ת	Tau	Thr	LOU	Luc	Λen	Ile	Leu	
120 121	ASII	ser	35	GIU	ASII	1111	MEC	40	міа	пец	1111	пеи	цу5 45	ASD	116	пеп	
122			7.7					40					13				
123	Asn	Glv	Thr	Phe	Ser	Tvr	Lvs	Thr	Phe	Phe	Pro	Asn	Trp	Ile	Ser	Glv	
124		50				- 1 -	55					60				1	
125																	
126	Gln	Glu	Tyr	Leu	His	Gln	Ser	Ala	Asp	Asn	Asn	Ile	Val	Leu	Tyr	Asn	
127	65		_			70					75					80	
128																	
129	Ile	Glu	Thr	Gly		Ser	Tyr	Thr	Ile		Ser	Asn	Arg	Thr	Met	Lys	
130					85					90					95		
131	a	**- 1	3		a	3	m	al	T	Q	D	7	7	~1 <u>~</u>	Db	170.1	
132 133	ser	vai	Asn	100	ser	ASI	Tyr	GIY	105	ser	Pro	Asp	Arg	110	Phe	Val	
134				100					105					110			
135	Tvr	Len	Glu	Ser	Asp	Tvr	Ser	Lvs	Leu	Trp	Ara	Tvr	Ser	Tvr	Thr	Ala	
136	- / -		115			-1-		120			5	-1-	125	- 1 -			
137																	
138	Thr	Tyr	Tyr	Ile	Tyr	Asp	Leu	Ser	Asn	Gly	Glu	Phe	Val	Arg	Gly	Asn	
139		130					135					140					
140																	
141		Leu	Pro	Arg	Pro		Gln	Tyr	Leu	Cys		Ser	Pro	Val	Gly		
142	145					150					155					160	
143	T	.	3 1 -		**- 1		a1	3	3	т1.	m	T	T	~1 m	7	Dec	
144	Lys	Leu	Ата	Tyr		Tyr	GIN	Asn	Asn		Tyr	Leu	ьуs	GIN	Arg	Pro	
145 146					165					170					175		
147	Glv	Δsn	Pro	Pro	Phe	Gln	Tle	Thr	Phe	Asn	Glv	Ara	Glu	Asn	Lys	Tle	
148	Cry	ASP	110	180	1110	O 1 11			185		1	9	CIU	190	-,5		
149																	
150	Phe	Asn	Gly	Ile	Pro	Asp	Trp	Val	Tyr	Glu	Glu	Glu	Met	Leu	Pro	Thr	
151			195			=	-	200					205				
152																	

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														II	VFUI	SEI: S
153 154	Lys	Tyr 210	Ala	Leu	Trp	Trp	Ser 215	Pro	Asn	Gly	Lys	Phe 220	Leu	Ala	Tyr	Ala
155 156 157	Glu 225	Phe	Asn	Asp	Lys	Asp 230	Ile	Pro	Val	Ile	Ala 235	Tyr	Ser	Tyr	Tyr	Gly 240
158 159 160	Asp	Glu	Gln	Tyr	Pro 245	Arg	Thr	Ile	Asn	Ile 250	Pro	Tyr	Pro	Lys	Ala 255	Gly
161 162 163	Ala	Lys	Asn	Pro 260	Val	Val	Arg	Ile	Phe 265	Ile	Ile	Asp	Thr	Thr 270	Tyr	Pro
164 165 166 167	Ala	Tyr	Val 275	Gly	Pro	Gln	Glu	Val 280	Pro	Val	Pro	Ala	Met 285	Ile	Ala	Ser
168 169 170	Ser	Asp 290	Tyr	Tyr	Phe	Ser	Trp 295	Leu	Thr	Trp	Val	Thr 300	Asp	Glu	Arg	Val
171 172 173	Cys 305	Leu	Gln	Trp	Leu	Lys 310	Arg	Val	Gln	Asn	Val 315	Ser	Val	Leu	Ser	Ile 320
174 175 176	Cys	Asp	Phe	Arg	Glu 325	Asp	Trp	Gln	Thr	Trp 330	Asp	Cys	Pro	Lys	Thr 335	Gln
177 178 179	Glu	His	Ile	Glu 340	Glu	Ser	Arg	Thr	Gly 345	Trp	Ala	Gly	Gly	Phe 350	Phe	Val
180 181 182	Ser	Arg	Pro 355	Val	Phe	Ser	Tyr	Asp 360	Ala	Ile	Ser	Tyr	Tyr 365	Lys	Ile	Phe
183 184 185	Ser	Asp 370	Lys	Asp	Gly	Tyr	Lys 375	His	Ile	His	Tyr	Ile 380	Lys	Asp	Thr	Val
186 187 188	Glu 385	Asn	Ala	Ile	Gln	Ile 390	Thr	Ser	Gly	Lys	Trp 395	Glu	Ala	Ile	Asn	Ile 400
189 190 191	Phe	Arg	Val	Thr	Gln 405	Asp	Ser	Leu	Phe	Tyr 410	Ser	Ser	Asn	Glu	Phe 415	Glu
192 193 194	Glu	Tyr	Pro	Gly 420	Arg	Arg	Asn	Ile	Tyr 425	Arg	Ile	Ser	Ile	Gly 430	Ser	Tyr
195 196 197	Pro	Pro	Ser 435	Lys	Lys	Cys	Val	Thr 440	Cys	His	Leu	Arg	Lys 445	Glu	Arg	Cys
198 199 200	Gln	Tyr 450	Tyr	Thr	Ala	Ser	Phe 455	Ser	Asp	Tyr	Ala	Lys 460	Tyr	Tyr	Ala	Leu
201 202 203	Val 465	Cys	Tyr	Gly	Pro	Gly 470	Ile	Pro	Ile	Ser	Thr 475	Leu	His	Asp	Gly	Arg 480
204 205	Thr	Asp	Gln	Glu	Ile 485	Lys	Ile	Leu	Glu	Glu 490	Asn	Lys	Glu	Leu	Glu 495	Asn

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206																
207 208 209	Ala	Leu	Lys	Asn 500	Ile	Gln	Leu	Pro	Lys 505	Glu	Glu	Ile	Lys	Lys 510	Leu	Glu
210 211 212	Val	Asp	Glu 515	Ile	Thr	Leu	Trp	Tyr 520	Lys	Met	Ile	Leu	Pro 525	Pro	Gln	Phe
213 214 215	Asp	Arg 530	Ser	Lys	Lys	Tyr	Pro 535	Leu	Leu	Ile	Gln	Val 540	Tyr	Gly	Gly	Pro
216 217 218	Cys 545	Ser	Gln	Ser	Val	Arg 550	Ser	Val	Phe	Ala	Val 555	Asn	Trp	Ile	Ser	Tyr 560
219 220	Leu	Ala	Ser	Lys	Glu 565	Gly	Met	Val	Ile	Ala 570	Leu	Val	Asp	Gly	Arg 575	Gly
221 222 223	Thr	Ala	Phe	Gln 580		Asp	Lys	Leu	Leu 585		Ala	Val	Tyr	Arg 590		Leu
224 225 226	Gly	Val	Tyr 595	Glu	Val	Glu	Asp	Gln 600	Ile	Thr	Ala	Val	Arg 605	Lys	Phe	Ile
227 228 229	Glu	Met 610	Gly	Phe	Ile	Asp	Glu 615	Lys	Arg	Ile	Ala	Ile 620	Trp	Gly	Trp	Ser
230 231 232	Tyr 625	Gly	Gly	Tyr	Val	Ser 630	Ser	Leu	Ala	Leu	Ala 635	Ser	Gly	Thr	Gly	Leu 640
233 234 235	Phe	Lys	Cys	Gly	Ile 645	Ala	Val	Ala	Pro	Val 650	Ser	Ser	Trp	Glu	Tyr 655	Tyr
236 237 238	Ala	Ser	Val	Tyr 660	Thr	Glu	Arg	Phe	Met 665	Gly	Leu	Pro	Thr	Lys 670	Asp	Asp
239 240 241	Asn	Leu	Glu 675	His	Tyr	Lys	Asn	Ser 680	Thr	Val	Met	Ala	Arg 685	Ala	Glu	Tyr
242 243 244	Phe	Arg 690	Asn	Val	Asp	Tyr	Leu 695	Leu	Ile	His	Gly	Thr 700	Ala	Asp	Asp	Asn
245 246 247	Val 705	His	Phe	Gln	Asn	Ser 710	Ala	Gln	Ile	Ala	Lys 715	Ala	Leu	Val	Asn	Ala 720
248 249 250	Gln	Val	Asp	Phe	Gln 725	Ala	Met	Trp	Tyr	Ser 730	Asp	Gln	Asn	His	Gly 735	Leu
251 252 253	Ser	Gly	Leu	Ser 740	Thr	Asn	His	Leu	Tyr 745	Thr	His	Met	Thr	His 750	Phe	Leu
254 255 256 257 258	Lys	Gln	Cys 755	Phe	Ser	Leu	Ser	Asp 760								

SEQUENCE VERIFICATION REPORT PATENT APPLICATION US/09/265,606

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